

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 25.703 Seconds
 (without alignments)
 1104.206 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550

Sequence: 1 MLLVLLVLSWLBGGGSLA.....DTGVSILQTYDDILAKDCHCI 295

Scoring table: BLOSUM62

Gapopen 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR:79;*
 1: _pir1;*
 2: _pir2;*
 3: _pir3;*
 4: _pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1522.5	98.2	309	2 JC5697	placental transform
2	229	14.8	513	1 BMHU6	bone morphogenetic
3	221	14.3	372	2 C39364	GDF-1, embryonic gr
4	216	13.9	510	2 A54798	Vg-1-related prote
5	215.5	13.9	365	2 T43286	ct-1 protein - Ca
6	212.5	13.7	402	2 A45056	osteogenic protein
7	212	13.7	354	2 S29718	gene nodal protein
8	208	13.4	371	2 S37618	vgr protein - rat
9	207	13.4	431	1 BMHU7	bone morphogenetic
10	206.5	13.3	454	1 BMHU5	bone morphogenetic
11	204	13.2	452	2 I49542	bone morphogenetic
12	204	13.2	360	2 A29619	Vg1 embryonic grow
13	204	13.2	430	2 JQ1184	osteogenic protein
14	202	13.0	313	2 I51284	bone morphogenetic
15	199	12.8	455	2 A43918	TGF-beta-related p
16	196	12.6	426	2 JH0690	bone morphogenetic
17	193	12.5	350	2 JCS241	activin beta B cha
18	189.5	12.2	441	2 S45284	growth/differentia
19	188	12.1	398	2 JH0687	bone morphogenetic
20	187	12.1	357	2 A39364	GDF-1 embryonic gr
21	186.5	12.0	588	2 A26158	decapentaplegic pr
22	183	11.8	398	2 JH0688	bone morphogenetic
23	182.5	11.8	515	2 S43296	bone morphogenetic
24	179	11.5	393	2 S37073	bone morphogenetic
25	177	11.4	436	2 B55452	cartilage-derived
26	176	11.4	408	2 S58791	bone morphogenetic
27	175	11.3	501	2 JC2347	growth/differentia
28	174.5	11.3	476	2 JC4646	bone morphogenetic
29	174	11.2	461	2 S52408	SPDVR1 protein - s

ALIGNMENTS

RESULT 1						
JC5697	placental transforming growth factor-beta homolog - human					
C;Species: Homo sapiens (man)						
C;Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 09-Jul-2004						
C;Accession: JC5697						
R;Yokoyama-Kobayashi, M.; Sekiki, M.; Sekine, S.; Kato, S.						
J. Biochem. 122, 622-626, 1997						
A;Title: Human cDNA encoding a novel TGF-beta superfamily protein highly expressed in 1						
A;Reference number: JC5697; MUID: 98006316; PMID: 9348093						
A;Accession: JC5697						
A;Molecule type: mRNA						
A;Cross-references: UNIPROT:Q9BW0; DDBJ:AB000584						
A;Experimental source: fibrobloma						
C;Comment: This protein plays a role in reproduction.						
Query Match 98.2%; Score 1522.5; DB 2; Length 309;						
Best Local Similarity 99.0%; Pred. No. 1-309 <YOK>						
Matches 293; Conservative 0; Mismatches 2; Indels 1; Gaps 1;						
Query 1 MLLVLLVLSWLBGGGSLA.....DTGVSILQTYDDILAKDCHCI 59						
DB 14 MLLVLLVLSWLBGGGSLA.....DTGVSILQTYDDILAKDCHCI 73						
Qy 60 WEDNTDLYPAPAVRILTPEVRIGSGGHHLR1SRAALPGLPAPRLLRFLSPASPTAS 119						
Db 74 WEDNTDLYPAPAVRILTPEVRIGSGGHHLR1SRAALPGLPAPRLLRFLSPASPTAS 133						
Qy 120 RSMWDTPLRRLQSLAPAPALHLRLSPPLSPSQDQLAESSSSAPOLFLHLRQARER 179						
Db 134 RSMWDTPLRRLQSLAPAPALHLRLSPPLSPSQDQLAESSSSAPOLFLHLRQARER 193						
Qy 180 RRARARNGDHCPGSPGRCCRLLTPTASLEDLGNDWVLSPREYVTCMIGACPQFRAAN 239						
Db 194 RRARARNGDHCPGSPGRCCRLLTPTASLEDLGNDWVLSPREYVTCMIGACPQFRAAN 253						
Qy 240 MHAQIKTSLHLRKLKDPTVPAACCVYDASYNPMVLIQTKDTSVSLQTYDDILAKDCHCI 295						
Db 254 MHAQIKTSLHLRKLKDPTVPAACCVYDASYNPMVLIQTKDTSVSLQTYDDILAKDCHCI 309						

RESULT 2

BMHU6

bone morphogenetic protein 6 precursor - human

C;Species: Homo sapiens (man)

C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: B39263

R;Celetti, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Woz

Proc. Natl. Acad. Sci. U.S.A. 87, 9841-9847, 1990

A;Title: Identification of transforming growth factor beta family members present in bo

A;Reference number: A39263; MUID: 9108608; PMID: 2263636

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OM protein - protein search, using SW model

Run on: June 7, 2005, 14:44:20 ; Search time 99.8911 Seconds
(without alignments)
1142.187 Million cell updates/sec

Title: US-10-009-431-3

Perfect score: 1550
Sequence: 1 MLLVLVLVSLWLPHGALSIA. DTGVSLSQTYDDLLAKDCHCT 295

Scoring table: BLOSUM62

Gapext 0.5
Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: GeneseqP19808:*

2: GeneseqP19908:*

3: GeneseqP20008:*

4: GeneseqP20018:*

5: GeneseqP20028:*

6: GeneseqP20038:*

7: GeneseqP2003bs:*

8: GeneseqP20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1550	100.0	295	4	AAB36557	Aab36557 Human GDF
2	1550	100.0	308	2	AAR77097	Aar77097 Human TGF
3	1550	100.0	308	2	AAW10662	AAw10662 Human TGF
4	1550	100.0	308	3	AAB26122	Aab26122 Human TGF
5	1550	100.0	308	5	AB009174	Ab009174 Human NAG
6	1550	100.0	308	5	Ae13538	Ae13538 Human mac
7	1550	100.0	308	6	Adl1070	Adl1070 Human cDN
8	1550	100.0	308	8	ADE77027	Ade77027 Human pro
9	1550	100.0	308	8	Adl12720	Adl12720 Human ste
10	1546	99.7	308	2	AAR84710	Aar84710 Human emb
11	1546	99.7	308	2	AAW10673	Aaw10673 Human TGF
12	1546	99.7	308	2	AAW10666	Aaw10666 Human TGF
13	1546	99.7	308	2	Aaw10672	Aaw10672 Human TGF
14	1546	99.7	308	2	AAW10670	Aaw10670 Human apo
15	1546	99.7	308	2	AAW10668	Aaw10668 Human TGF
16	1546	99.7	308	2	AAW10671	Aaw10671 Human TGF
17	1546	99.7	308	2	AAW48672	Aaw48672 GR-2H pro
18	1546	99.7	308	7	AD163071	Ad163071 Human apo
19	1546	99.7	308	8	ABm82070	Abm82070 Tumour-as
20	1542	99.5	308	2	ADG71946	Adg71946 Human NOV
21	1542	99.5	308	8	AAB36553	Aab36553 Human pro
22	1538	99.2	295	2	AAW02613	Aaw02613 Human TGF
23	1537	99.2	308	2	AAW10670	Aaw10670 Human TGF
24	1537	99.2	308	2	AAW10659	Aaw10659 Human mac
25	1537	99.2	308	5	AAE13539	Aae13539 Human mac

Hom sapiens.

OS

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PN

XX

PD

XX

PP

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PR

XX

PR

XX

PA

XX

PA

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PI

XX

DR

XX

DR

XX

XX

XX

XX

XX

XX

ALIGNMENTS

RESULT 1
AAB36557

ID AAB36557 standard; protein; 295 AA.

AC AAB36557;

XX

DT 07-MAR-2001 (first entry)

XX

Human GDF-15 pre-mature protein sequence.

KW Human; growth/differentiation factor; GDF; hGDF-15; neuroprotective; transforming growth factor beta; TGF-beta; neurotrophic; diagnosis; neurodegenerative; detection; dopaminergic; cerebroprotective; stroke; antiParkinsonian; neurotropic; neuroprotective; antidepressant; dementia; neuroleptic; neurodegenerative disorder; neurological disorder; psychological disorder; Parkinson's disease; central nervous system; infection; Alzheimer's disease; schizophrenia; meningitis.

XX

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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 9.75842 Seconds
(without alignments)
11.04.306 Million cell updates/sec

Title: US-10-009-431-4

Perfect score: 624
Sequence: 1 ARNGDHCPGLPGRCCRHLTV.....DTGVSLQTYDDILAKDCHCI 112Scoring table: BL2SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79;*
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	624	100.0	309	2	JC5697		placental transfer
2	201	32.2	365	2	A43918		cet-1 protein - Ca
3	195	31.2	455	2	A43918		TGF-beta related p
4	192	30.8	430	2	JQ1184		osteoigenic protein
5	191	30.6	513	1	BMHU6		bone morphogenetic
6	190	30.4	426	2	JH0690		bone morphogenetic
7	188	30.1	207	2	S37618		vgr protein - rat
8	188	30.1	313	2	I51284		bone morphogenetic
9	188	30.1	431	1	BMHU7		bone morphogenetic
10	188	30.1	452	2	I49542		bone morphogenetic
11	188	30.1	454	1	BMHU5		bone morphogenetic
12	188	30.1	510	2	A54798		Vg-1 related prote
13	185	29.6	360	2	A29619		Vg1 embryonic grow
14	179.5	28.8	151	2	S34296		bone morphogenetic
15	176	28.2	372	2	C39364		GDF-1 embryonic gr
16	175	28.0	402	2	A45056		osteoigenic protein
17	174	27.9	441	2	S45284		growth/differentiation
18	170	27.2	588	2	A26158		decapentaplegic pr
19	169.5	27.2	495	2	S43294		bone morphogenetic
20	169.5	27.2	501	2	JC2347		growth/differentiation
21	169.5	27.2	501	2	A55452		cartilage-derived
22	167	26.8	354	2	S29718		gene nodal protein
23	165	26.4	61	2	S52408		SPDR1 protein - s
24	163.5	26.2	125	2	S43295		bone morphogenetic
25	163	26.1	357	2	A39364		GDF-1 embryonic gr
26	162.5	26.0	366	2	A46607		growth/differentiation
27	157.5	25.2	366	2	A45402		transforming growth
28	156	25.0	436	2	B55452		cartilage-derived
29	150.5	24.1	350	2	JC5241		activin beta B cha

ALIGNMENTS

Query	Match	Score	DB	Length	Comments
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	112	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
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Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
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Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
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Qy	1 ARNGDHCPGLPGRCCRHLTVRASLDLGWADWVLSPREYQTMCTGACPSQFRANMHAQ 60	100.0%	DB	198	Best Local Similarity 100.0%; Pred. No. 2.3e-55; N mismatches 0; Indels 0; Gaps 0; Cross-references: UNIPROT:Q9BWAO; DDBJ:AB000584
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listings first 45 summaries
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4: geneset2018::

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8: GeneSeqP2004B:*

COMMUNES

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4	624	100.0	141	2	AAW1674	TGF-beta-
5	624	100.0	154	2	AAW1665	Human TGF
6	624	100.0	203	2	AAW1664	Aaw10664
7	624	100.0	283	8	ADJ87287	Human G
8	624	100.0	295	4	AAB31557	Human GDF
9	624	100.0	308	2	AAR77097	Aar87710
10	624	100.0	308	2	AAR8710	Human emb
11	624	100.0	308	2	AAW1673	Human TGF
12	624	100.0	308	2	AAW1666	Human TGF
13	624	100.0	308	2	AAW1672	Aaw10672
14	624	100.0	308	2	AAW1662	Human TGF
15	624	100.0	308	2	AAW1668	Human TGF
16	624	100.0	308	2	AAW1667	Aaw10667
17	624	100.0	308	2	AAW10671	Human TGF
18	624	100.0	308	2	AAB48672	Aaw48672
19	624	100.0	308	3	AAB26122	BP-2H pro
20	624	100.0	308	5	ABB09174	Aab26122
21	624	100.0	308	5	AAE13538	Human NAG
22	624	100.0	308	6	ADA11070	Aae13538
23	624	100.0	308	7	AD163071	Human apo
24	624	100.0	308	8	ADE77027	Aad112220
25	624	100.0	308	9	AD112220	Ade77027

XX	(ASAH) ASAHI KASEI KOGYO KK.
PA	
XX	
DR	WPI: 1995-380074/49.
DR	N-FSDB; AAT05177.
XX	
PT	A new protein for the treatment
PT	production of active oxygen is
XX	
PS	Claim 1; Page 2; 26pp; Japanese
XX	
CC	The present sequence is that of
CC	from normal diploid cells of
CC	inhibits production of active
CC	treatment and prevention of by
XX	
SQ	Sequence 112 AA;
XX	
Qy	Query Match 100.0%;
	Best local Similarity 100.0%;
	Matches 112; Conservative 0;
Db	1 ARNGDHCPLGPGRCCPRLHTV
	1 ARNGDHCPLGPGRCCPRLHTV

ALIGNMENTS

RESULT 1
AAR84709

XX AAR84709;
 AC
 XX
 DT 23-MAY-1996 (first entry)
 DS Human embryonal lung mature protein
 XX
 KW Eosinophil inhibitor; active oxyge
 KW embryonal lung.

OS	Homo sapiens.	
XX		
PN	JP07258293-A.	
XX		
PD	09-OCT-1995.	
XX		
PP	23-MAR-1994;	94JP-00052225.
XX		
PR	23-MAR-1994;	94JP-00052225.
XX		
PA	(ASAH) ASAHI KASEI KOGYO KK.	
XX		
DR	WPI; 1995-380074/49.	
DR	N-PSDB; AAT05177.	
XX		
PT	A new protein for the treatment of bronchial asthma - inhibits the	

XX
PS Claim 1; Page 2; 26pp; Japanese.
XX
CC The present sequence is that of a 112 amino acid mature protein isolated
CC from normal diploid cells of human embryonal lung tissue. The protein
CC inhibits production of active oxygen in eosinophils and is useful for
CC treatment and prevention of bronchial asthma
XX
SQ Sequence 112 AA;

Query	Match	Score	DB	Length	;
Qy	1 ARNGHCPGLPGRCCRLHTYRASLFDLGMDAWLSPREYQVTMCGACPSQRAANMHAQ	100.0%	DB 2;	Length 112;	
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			Ms matches 0;	Indels 0;	Gaps 0;
			Matches 112;	Conservative 0;	

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 7, 2005, 14:47:41 ; Search time 10.2851 Seconds
 (without alignments)
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Title: US-10-009-431-4_COPY_14_111
 Perfect score: 541

Sequence: 1 CCRLHTVRAASLDLGWADWV.....TDTGVSILQTYDDLLAKDCHC 98

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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 Listing First 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	541	100.0	112	3 US-08-927-133-8	Sequence 8, Appli
3	541	100.0	112	3 US-08-927-433-10	Sequence 1, Appli
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5	541	100.0	308	3 US-08-927-133-9	Sequence 9, Appli
6	541	100.0	308	3 US-08-775-982-4	Sequence 4, Appli
7	541	100.0	308	3 US-08-775-982-6	Sequence 6, Appli
8	541	100.0	308	4 US-09-276-000-6	Sequence 6, Appli
9	541	100.0	308	4 US-09-97-594-449	Sequence 449, Appli
10	541	100.0	308	4 US-09-919-039-192	Sequence 192, Appli
11	541	100.0	314	4 US-09-949-016-1011.8	Sequence 1011.8, Appli
12	537	99.3	295	2 US-08-11-60A-2	Sequence 2, Appli
13	537	99.3	295	4 US-09-361-741-2	Sequence 2, Appli
14	537	99.3	295	4 US-09-461-418-2	Sequence 2, Appli
15	535	98.9	308	4 US-09-19-016-6559	Sequence 6559, Appli
16	407	75.2	115	4 US-09-163-331-2	Sequence 2, Appli
17	195	36.0	117	4 US-09-374-958C-9	Sequence 69, Appli
18	195	36.0	139	4 US-09-374-958C-68	Sequence 68, Appli
19	195	36.0	438	2 US-08-159-346-14	Sequence 14, Appli
20	195	36.0	438	3 US-08-889-419-14	Sequence 14, Appli
21	195	36.0	438	3 US-08-840-542-14	Sequence 14, Appli
22	195	36.0	438	5 PCT-US3-07189-14	Sequence 14, Appli
23	193	35.7	102	4 US-09-374-958C-53	Sequence 53, Appli
24	193	35.7	430	1 US-07-841-616-25	Sequence 25, Appli
25	193	35.7	430	1 US-07-901-703-9	Sequence 9, Appli
26	193	35.7	430	3 US-08-445-467-19	Sequence 19, Appli
27	193	35.7	430	4 US-09-464-206-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
 US-08-775-882-2
 ; Sequence 2, Application US/08775882
 ; Patent No. 618002
 ; GENERAL INFORMATION:
 ; APPLICANT: KATO, Seishi
 ; APPLICANT: OH, Suwan
 ; APPLICANT: SERINE, Shingo
 ; APPLICANT: SAKKI, Mihiro
 ; APPLICANT: KOBAYASHI, Midori
 ; APPLICANT: YADA, Mika
 ; APPLICANT: OHMORI, Tomoko
 ; TITLE OF INVENTION: HUMAN NOVEL CDNA, TGF-BETA SUPERFAMILY PROTEIN ENCODED THEREBY AND THE USE AS IMMUNOSUPPRESSIVE AGENT
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20000-5109
 ; COMPUTER READEABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIN Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/775-882
 ; FILING DATE: 02-JAN-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/390,207
 ; FILING DATE: 16-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/379,441
 ; FILING DATE: 03-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 5-61431
 ; FILING DATE: 26-FEB-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 4-327619
 ; FILING DATE: 13-NOV-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 4-208077
 ; FILING DATE: 04-AUG-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WEGNER, Harold C.

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RESULT 1

US-10-373-581-4

Sequence 4, Application US/10373581
Publication No. US20030211541A1

GENERAL INFORMATION:

APPLICANT: Lee et al., Se-Jin
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-14
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/373,581
FILING DATE: 24-Feb-2003
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/626,185
FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hale, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/088001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5599
INFORMATION FOR SEQ ID NO: 4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	541	100.0	308	9	Sequence 76, Appli
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5	541	100.0	308	10	Sequence 188, Appli
6	541	100.0	308	13	Sequence 192, Appli
7	541	100.0	308	15	Sequence 6, Appli
8	541	100.0	308	15	Sequence 1, Appli
9	541	100.0	308	16	Sequence 2, Appli
10	537	99.3	295	14	Sequence 2, Appli
11	537	99.3	295	14	Sequence 327, Appli
12	535	98.9	308	14	Sequence 327, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMATES

Result No.	Score	Query			DB	ID	Description
		Match	Length	ID			
1	541	100.0	119	15	US-10-373-581-4		Sequence 4, Appli
2	541	100.0	283	15	US-10-211-683-76		Sequence 76, Appli
3	541	100.0	308	9	US-09-276-600-6		Sequence 6, Appli
4	541	100.0	308	9	US-09-981-353-188		Sequence 188, APP
5	541	100.0	308	10	US-09-919-039-192		Sequence 192, APP
6	541	100.0	308	13	US-10-000-628-6		Sequence 6, Appli
7	541	100.0	308	15	US-10-251-597-1		Sequence 1, Appli
8	541	100.0	308	15	US-10-257-597-2		Sequence 2, Appli
9	541	100.0	308	16	US-10-425-115-229584		Sequence 229584, Appli
10	537	99.3	295	9	US-09-361-741-2		Sequence 2, Appli
11	537	99.3	295	14	US-10-270-377-2		Sequence 2, Appli
12	535	98.9	308	14	US-10-205-823-327		Sequence 327, APP

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Post-processing:	Minimum Match 0% Maximum Match 100% Listings first 45 summaries			
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Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Match	Length	DB ID
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2	541	100.0	308	2 Q9BWA0
3	407	75.2	303	1 GDFP_MOUSE
4	399	75.2	303	2 Q6NK63
5	239	73.8	303	1 GDFP_RAT
6	239	44.2	387	2 Q869H8
7	201	37.2	365	2 Q02424
8	200	37.2	365	2 Q76514
9	200	37.0	424	2 Q6P4J4
10	195	36.0	288	2 Q6PUBL
11	194	35.9	441	2 Q6PUDL
12	194	35.9	441	2 Q7PZI7
13	192	35.5	424	2 Q9YGH7
14	191	35.3	430	1 BMP6_HUMAN
15	191	35.3	513	1 BMP6_TURMAN
16	189	34.9	373	2 Q90723
17	189	34.9	373	2 Q98890
18	188	34.8	207	1 BMP6 RAT
19	188	34.8	350	2 Q66KL4
20	188	34.8	426	1 BMP7_XENLA
21	188	34.8	426	2 Q6PF75
22	188	34.8	435	2 Q8BRW3
23	188	34.8	506	2 Q811SA
24	188	34.8	510	1 BMP6 MOUSE
25	187	34.6	313	2 Q91403
26	187	34.6	398	2 Q918T6
27	187	34.6	424	2 Q6F2B8
28	187	34.6	431	1 BMP7_HUMAN
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Scoring table:	BLOSUM62	Gapopen 10.0 , Gapext 0.5	1612378 seqs, 512079187 residues	Total number of hits satisfying chosen parameters: 1612378
Searched:	1612378 seqs, 512079187 residues			
Post-processing:	Minimum Match 0% Maximum Match 100% Listings first 45 summaries			
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Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Match	Length	DB ID
1	541	100.0	308	1 GDFP_HUMAN
2	541	100.0	308	2 Q9BWA0
3	407	75.2	303	1 GDFP_MOUSE
4	399	73.8	303	1 GDFP_RAT
5	239	44.2	387	2 Q869H8
6	239	37.2	365	2 Q02424
7	201	37.2	365	2 Q76514
8	200	37.0	424	2 Q6P4J4
9	195	36.0	288	2 Q6PUBL
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11	194	35.9	441	2 Q7PZI7
12	194	35.9	441	2 Q9YGH7
13	192	35.5	424	2 Q90723
14	191	35.3	430	1 BMP6_HUMAN
15	191	35.3	513	1 BMP6_TURMAN
16	189	34.9	373	2 Q98890
17	189	34.9	373	2 Q66KL4
18	188	34.8	207	1 BMP6 RAT
19	188	34.8	350	2 Q04906
20	188	34.8	426	1 BMP7_XENLA
21	188	34.8	426	2 Q6PF75
22	188	34.8	435	2 Q8BRW3
23	188	34.8	506	2 Q811SA
24	188	34.8	510	1 BMP6 MOUSE
25	187	34.6	313	2 Q91403
26	187	34.6	398	2 Q918T6
27	187	34.6	424	2 Q6F2B8
28	187	34.6	431	1 BMP7_HUMAN
29	187	34.6	436	1 60A_DICROVI
30	187	34.6	455	1 60A_DROME
31	186	34.4	446	2 Q7T2B8

Scoring table:	BLOSUM62	Gapopen 10.0 , Gapext 0.5	1612378 seqs, 512079187 residues	Total number of hits satisfying chosen parameters: 1612378
Searched:	1612378 seqs, 512079187 residues			
Post-processing:	Minimum Match 0% Maximum Match 100% Listings first 45 summaries			
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
Result No.	Score	Match	Length	DB ID
1	541	100.0	308	1 GDFP_HUMAN
2	541	100.0	308	2 Q9BWA0
3	407	75.2	303	1 GDFP_MOUSE
4	399	73.8	303	1 GDFP_RAT
5	239	44.2	387	2 Q869H8
6	239	37.2	365	2 Q02424
7	201	37.2	365	2 Q76514
8	200	37.0	424	2 Q6P4J4
9	195	36.0	288	2 Q6PUBL
10	194	35.9	441	2 Q6PUDL
11	194	35.9	441	2 Q7PZI7
12	194	35.9	441	2 Q9YGH7
13	192	35.5	424	2 Q90723
14	191	35.3	430	1 BMP6_HUMAN
15	191	35.3	513	1 BMP6_TURMAN
16	189	34.9	373	2 Q98890
17	189	34.9	373	2 Q66KL4
18	188	34.8	207	1 BMP6 RAT
19	188	34.8	350	2 Q04906
20	188	34.8	426	1 BMP7_XENLA
21	188	34.8	426	2 Q6PF75
22	188	34.8	435	2 Q8BRW3
23	188	34.8	506	2 Q811SA
24	188	34.8	510	1 BMP6 MOUSE
25	187	34.6	313	2 Q91403
26	187	34.6	398	2 Q918T6
27	187	34.6	424	2 Q6F2B8
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Scoring table:	BLOSUM62	Gapopen 10.0 , Gapext 0.5	1612378 seqs, 512079187 residues	Total number of hits satisfying chosen parameters: 1612378
Searched:	1612378 seqs, 512079187 residues			
Post-processing:	Minimum Match 0% Maximum Match 100% Listings first 45 summaries			
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
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1	541	100.0	308	1 GDFP_HUMAN
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5	239	44.2	387	2 Q869H8
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13	192	35.5	424	2 Q90723
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Scoring table:	BLOSUM62	Gapopen 10.0 , Gapext 0.5	1612378 seqs, 512079187 residues	Total number of hits satisfying chosen parameters: 1612378
Searched:	1612378 seqs, 512079187 residues			
Post-processing:	Minimum Match 0% Maximum Match 100% Listings first 45 summaries			
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *			
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES				
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4	399	73.8	303	1 GDFP_RAT
5	239	44.2	387	2 Q869H8
6	239	37.2	365	2 Q02424
7	201	37.2	365	2 Q76514
8	200	37.0	424	2 Q6P4J4
9	195	36.0	288	2 Q6PUBL
10	194	35.9	441	2 Q6PUDL
11	194	35.9	441	2 Q7PZI7
12	194	35.9	441	2 Q9YGH7
13	192	35.5	424	2 Q90723
14	191	35.3	430	1 BMP6_HUMAN
15	191	35.3	513	1 BMP6_TURMAN
16	189	34.9	373	2 Q98890
17	189	34.9	373	2 Q66KL4
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20	188	34.8	426	1 BMP7_XENLA
21	188	34.8	426	2 Q6PF75
22	188	34.8	435	2 Q8BRW3
23	188	34.8	506	2 Q811SA
24	188	34.8	510	1 BMP6 MOUSE
25	187	34.6	313	2 Q91403
26	187	34.6	398	2 Q918T6
27	187	34.6	424	2 Q6F2B8
28	187	34.6	431	1 BMP7_HUMAN
29	187	34.6	436	1 60A_DICROVI
30	187	34.6	455	1 60A_DROME
31	186	34.4	446	2 Q7T2B8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 7, 2005, 14:46:46 ; Search time 8.53861 Seconds

(without alignments)
1104.306 Million cell updates/sec

Title: US-10-009-431-4_COPY_14_111

Perfect score: 541

Sequence: 1 CCRHLTYRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC 98

Scoring table: BLOSSM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lassing first 45 summaries

Database : PIR_79;*

1: Piri;*

2: Piri2;*

3: Piri3;*

4: Piri4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	541	100.0	309	2	JC5697	placental transfer
2	201	37.2	365	2	J01286	cat-1 protein - Ca
3	191	35.3	430	2	J01184	osteogenic protein
4	191	35.3	513	1	BMHU5	bone morphogenetic
5	188	34.8	207	2	S37618	vgr protein - rat
6	188	34.8	426	2	JH0690	bone morphogenetic
7	188	34.8	510	2	A54798	Vg-1-related prote
8	187	34.6	313	1	151284	bone morphogenetic
9	187	34.6	431	1	BMHU7	bone morphogenetic
10	187	34.6	455	2	A43918	TGF-beta-related p
11	184	34.0	452	2	149542	bone morphogenetic
12	184	34.0	454	1	BMHU5	bone morphogenetic
13	181	33.5	360	2	A29619	Vg1 embryonic grow
14	173	32.0	151	2	S43296	bone morphogenetic
15	173	32.0	402	2	A45056	osteogenic protein
16	172	31.8	441	2	S45284	growth/differentia
17	170	31.4	588	2	A26158	decapentaplegic pr
18	168	31.1	495	2	S43294	bone morphogenetic
19	168	31.1	501	2	JC2347	growth/differentia
20	168	31.1	501	2	A5452	cartilage-derived
21	164.5	30.4	354	2	S29718	gene nodal protein
22	163	30.1	461	2	S552408	SPDV1 protein - S
23	161	29.8	125	2	S43295	bone morphogenetic
24	160.5	29.7	366	2	A46607	growth/differentia
25	159	29.4	372	2	C39364	GDF-1 embryonic gr
26	156	28.8	436	2	B35452	cartilage-derived
27	155.5	28.7	366	2	A45402	transforming growth
28	152.5	28.2	357	2	A39364	GDF-1 embryonic gr
29	150.5	27.8	350	2	JC5241	activin beta B cha

ALIGNMENTS

Query	Match	Score	541	DB 2;	Length	309;	
Qy	1	100.0%	Score	541;	Pred. No.	5.8e-51;	
Qy	98	Conservative	0;	Mismatches	0;	Indels	0;
Qy	98	Local Similarity	100.0%	Best	Matches	98;	
Db	211	CCCRHTVRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC	98	Cross-references	UNIPROT:Q9BWAQ;	DBJ:AB000584	
Db	271	CCRLHTVRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC	98	Experimental source	Fibrocarcina		
Db	271	CCRLHTVRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC	98	Comment	This protein plays a role in reproduction.		
Qy	1	CCRLHTVRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC	98	Query	1	CCRLHTVRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC	
Db	211	CCRLHTVRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC	98	Match	100.0%	Score	541;
Db	271	CCRLHTVRASLLEDLGWADWW.....TDTGVSLQTYDDILAKDCHC	98	5	DB 2;	Length	309;

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OM protein - protein search, using sw model

Run on: June 7, 2005, 15:29:15 ; Search time 63 Seconds (without alignments)

601.627 Million cell updates/sec

Title: US-10-009-431-4_COPY_14_111

Perfect score: 541

Sequence: 1 CCRLHTVRASLEDLGWADKV.....TDTGVSLQTYDDILAKDCHC 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: GeneseqP1900s:*

2: GeneseqP1900s:*

3: GeneseqP2000s:*

4: GeneseqP2001s:*

5: GeneseqP2002s:*

6: GeneseqP2003as:*

7: GeneseqP2003bs:*

8: GeneseqP2004s:*

Result No.	Score	Query	Match	Length	DB ID	Description
1	541	100.0	112	2	AAR84709	Human emb
2	541	100.0	112	4	ABb36558	Human GDF
3	541	100.0	119	2	Aaw31509	Growth di
4	541	100.0	141	2	Aaw10674	TGF-beta
5	541	100.0	154	2	Aaw10665	Human TGF
6	541	100.0	203	2	Aaw10664	Human TGF
7	541	100.0	283	8	Aab87287	Human G P
8	541	100.0	295	4	Abb36557	Human GDF
9	541	100.0	308	2	Aar77097	Human TGF
10	541	100.0	308	2	AAR84710	Human emb
11	541	100.0	308	2	Aaw10673	Human TGF
12	541	100.0	308	2	Aaw10666	Human TGF
13	541	100.0	308	2	Aaw10670	Human TGF
14	541	100.0	308	2	Aaw10672	Human TGF
15	541	100.0	308	2	Aaw10669	Human TGF
16	541	100.0	308	2	Aaw10662	Human TGF
17	541	100.0	308	2	Aaw10668	Human TGF
18	541	100.0	308	2	Aaw10667	Human TGF
19	541	100.0	308	2	Aaw10671	Human TGF
20	541	100.0	308	2	Aaw48672	GP-2H pro
21	541	100.0	308	3	AAB26122	Human TGF
22	541	100.0	308	5	ABb09174	
23	541	100.0	308	5	Aae13538	Human NAG
24	541	100.0	308	5	Aae13539	Human mac
25	541	100.0	308	6	Ada11070	Human CDN

ALIGNMENTS

RESULT 1						
ID	AAR84709	standard; protein; 112 AA.	XX	XX	AC	XX
ID	AAR84709	standard; protein; 112 AA.	XX	XX	AC	XX
XX	AAR84709;		XX	XX	XX	XX
XX			DT	23-MAY-1996	(first entry)	XX
XX			DE		Human embryonal lung mature protein.	XX
XX			DE		Eosinophil; inhibitor; active oxygen production; bronchial asthma; human; embryonal lung.	XX
XX			OS		Homo sapiens.	OS
XX			PN		JP07258293-A.	PN
XX			XX			XX
PD			PD	09-OCT-1995.		PD
XX			XX			XX
PF			PF	23-MAR-1994;	94JP-00052225.	PF
XX			PR	23-MAR-1994;	94JP-00052225.	PR
XX			XX		(ASAHI) ASAHI KASEI KOGYO KK.	XX
XX			XX		WPI; 1995-380074/49.	XX
DR			DR		N-PSDB; AAT05177.	DR
XX			XX		A new protein for the treatment of bronchial asthma - inhibits the production of active oxygen in eosinophil(s).	XX
PT			PT			PT
XX			XX		Claim 1; Page 2; 25pp; Japanese.	XX
PS			PS		Sequence 112 AA;	PS
XX			XX		The present sequence is that of a 112 amino acid mature protein isolated from normal diploid cell(s) of human embryonal lung tissue. The protein inhibits production of active oxygen in eosinophils and is useful for treatment and prevention of bronchial asthma.	CC
SQ			SQ			SQ
Query Match			Query Match		100.0%; Score 541; DB 2;	Query Match
Best Local Similarity			Best Local Similarity		100.0%; Pred. No. 1-3e-51;	Best Local Similarity
Matches			Matches		0; Mismatches 0;	Matches
98;			98;		Indels 0; Gaps 0;	98;
Db			Db			Db
Qy			Qy		1 CCRRLHTVRASLEDLGWADKV.....TDTGVSLQTYDDILAKDCHC 98	Qy
Db			Db		14 CCRRLHTVRASLEDLGWADKV.....TDTGVSLQTYDDILAKDCHC 98	Db